

SEQUENCE LISTING

<110> ROSENTHAL, ANDRÉ et al.

<120> Nucleic Acid Molecules encoding proteins which influence bone development

<130> 0147-0211P

<140> PCT/EP99/02055

<141> 1999-03-26

<150> DE 198 13 799.0

<151> 1998-03-27

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<170> PatentIn Ver. 2.1

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Tyr Leu Val Gln Lys Val Val	Pro Met Leu Pro Arg	Leu Leu Cys Glu
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Glu Leu Cys Ser Leu Asn Pro	Met Thr Asp Lys	Leu Thr Phe Ser Val
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Ile Trp Lys Leu Thr Pro	Glu Gly Lys Ile Leu	Glu Glu Trp Phe Gly
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Ser Met Ile Glu Asn Pro	Thr Glu Lys Ile Pro	Glu Glu Glu Leu Pro
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Pro Ile Ser Pro Glu His	Ser Val Glu Glu Val His	Gln Ala Val Leu
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Asn Leu His Ser Ile Ala	Lys Gln Leu Arg Arg	Gln Arg Phe Val Asp
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gag gag ctg tgc agc ctc aac ccc atg tcc gac aag ctg acc ttc tct			191
Glu Glu Leu Cys Ser Leu Asn Pro Met Ser Asp Lys Leu Thr Phe Ser			
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gtg atc tgg aca ctg act cca gag ggc aag atc ctt gat gaa tgg ttt			239
Val Ile Trp Thr Leu Thr Pro Glu Gly Lys Ile Leu Asp Glu Trp Phe			
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Gly Arg Thr Ile Ile Arg Ser Cys Thr Lys Leu Ser Tyr Glu His Ala			
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Gln Ser Met Ile Glu Ser Pro Thr Glu Lys Ile Pro Ala Lys Glu Leu			
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Pro Pro Ile Ser Pro Glu His Ser Ser Glu Glu Val His Gln Ala Val			
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Leu Asn Leu His Gly Ile Ala Lys Gln Leu Arg Gln Gln Arg Phe Val			
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His Glu Thr Gly Leu Pro Gln Gly Cys His Ile Tyr Glu Tyr Arg Glu			
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agc aac aag ctc gtg gag gag ttc atg ctc ttg gcc aac atg gca gtg			575
Ser Asn Lys Leu Val Glu Glu Phe Met Leu Leu Ala Asn Met Ala Val			
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Asp Gln Met Gly Leu Pro Val Asp Phe Ser Ser Ala Gly Ala Leu Asn			
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aaa agc ctg acc caa aca ttt gga gat gac aag tac tca ctg gcc cgc			767
Lys Ser Leu Thr Gln Thr Phe Gly Asp Asp Lys Tyr Ser Leu Ala Arg			
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Lys Glu Val Leu Thr Asn Met Cys Ser Arg Pro Met Gln Met Ala Leu			
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Tyr Phe Cys Ser Gly Leu Leu Gln Asp Pro Ala Gln Phe Arg His Tyr			
	275	280	285
gcg ctc aat gtg ccc ctg tac aca cac ttc acc tcg ccc atc cgc cgc			911

Figure 4: The sequence of the DNA fragment (191-911) is shown. The sequence is written in the 5' to 3' direction. The sequence is: gag gag ctg tgc agc ctc aac ccc atg tcc gac aag ctg acc ttc tct Glu Glu Leu Cys Ser Leu Asn Pro Met Ser Asp Lys Leu Thr Phe Ser 50 55 60 239 gtg atc tgg aca ctg act cca gag ggc aag atc ctt gat gaa tgg ttt Val Ile Trp Thr Leu Thr Pro Glu Gly Lys Ile Leu Asp Glu Trp Phe 65 70 75 287 ggc cgg acc atc atc cgc tcc tgc acc aaa ctt agc tac gag cat gca Gly Arg Thr Ile Ile Arg Ser Cys Thr Lys Leu Ser Tyr Glu His Ala 80 85 90 95 335 cag agc atg att gaa agc cca act gag aaa atc cct gcg aaa gag ctg Gln Ser Met Ile Glu Ser Pro Thr Glu Lys Ile Pro Ala Lys Glu Leu 100 105 110 383 ccc ccc att tcc cca gag cat agc agc gag gag gta cac cag gcc gtc Pro Pro Ile Ser Pro Glu His Ser Ser Glu Glu Val His Gln Ala Val 115 120 125 431 ttg aat ctc cac gga att gcc aag cag tta cgc cag cag cgc ttt gtg Leu Asn Leu His Gly Ile Ala Lys Gln Leu Arg Gln Gln Arg Phe Val 130 135 140 479 gac ggc gca ctt cgt ttg gat cag cta aag ctt gct ttc act ctg gac Asp Gly Ala Leu Arg Leu Asp Gln Leu Lys Leu Ala Phe Thr Leu Asp 145 150 155 527 cac gag acc gga ttg cct caa gga tgt cat atc tat gag tac cgc gag His Glu Thr Gly Leu Pro Gln Gly Cys His Ile Tyr Glu Tyr Arg Glu 160 165 170 175 575 agc aac aag ctc gtg gag gag ttc atg ctc ttg gcc aac atg gca gtg Ser Asn Lys Leu Val Glu Glu Phe Met Leu Leu Ala Asn Met Ala Val 180 185 190 623 gcc cac aag atc cac cgc gcc ttc ccc gag cag gcc ctg ctg cgc cgg Ala His Lys Ile His Arg Ala Phe Pro Glu Gln Ala Leu Leu Arg Arg 195 200 205 671 cac ccc ccg ccc caa aca agg atg ctc agt gac ctg gtg gaa ttc tgc His Pro Pro Pro Gln Thr Arg Met Leu Ser Asp Leu Val Glu Phe Cys 210 215 220 719 gac cag atg ggg ctg ccc gtg gac ttc agc tcc gca gga gcc ctc aat Asp Gln Met Gly Leu Pro Val Asp Phe Ser Ser Ala Gly Ala Leu Asn 225 230 235 767 aaa agc ctg acc caa aca ttt gga gat gac aag tac tca ctg gcc cgc Lys Ser Leu Thr Gln Thr Phe Gly Asp Asp Lys Tyr Ser Leu Ala Arg 240 245 250 255 815 aag gag gtg ctc acc aac atg tgc tcc cgg ccc atg cag atg gca ctg Lys Glu Val Leu Thr Asn Met Cys Ser Arg Pro Met Gln Met Ala Leu 260 265 270 863 tac ttc tgc tgc ggg ctg ctg cag gac cca gcg cag ttc cgg cac tac Tyr Phe Cys Ser Gly Leu Leu Gln Asp Pro Ala Gln Phe Arg His Tyr 275 280 285 911 gcg ctc aat gtg ccc ctg tac aca cac ttc acc tcg ccc atc cgc cgc

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His	Cys	Asn	Asp	Arg	Arg	Met	Ala	Ser	Lys	Arg	Val	Gln	Glu	Leu	Ser		
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Country	Year	Value	Unit	Source
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Algeria	1971	1000	kg	FAO
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Algeria	1973	1000	kg	FAO
Algeria	1974	1000	kg	FAO
Algeria	1975	1000	kg	FAO
Algeria	1976	1000	kg	FAO
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Algeria	2048	1000	kg	FAO
Algeria</				

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Country	Year	Population	Area	Population Density	Area Density
Algeria	1960	10,000,000	2,381,472	420	0.17
Angola	1960	4,000,000	483,647	827	0.34
Argentina	1960	16,000,000	2,780,171	575	0.24
Australia	1960	7,000,000	7,726,141	90	0.04
Austria	1960	7,000,000	83,858	835	0.34
Belgium	1960	9,000,000	30,528	295	0.12
Brazil	1960	80,000,000	8,511,965	94	0.04
Canada	1960	24,000,000	9,970,610	241	0.10
China	1960	600,000,000	9,596,961	62	0.03
France	1960	21,000,000	543,845	388	0.16
Germany	1960	21,000,000	357,021	588	0.24
India	1960	360,000,000	3,287,263	110	0.05
Italy	1960	28,000,000	301,330	930	0.38
Japan	1960	100,000,000	377,915	265	0.11
Kenya	1960	10,000,000	224,961	44	0.02
Madagascar	1960	4,000,000	587,041	68	0.03
Mali	1960	10,000,000	1,240,192	81	0.03
Mexico	1960	24,000,000	1,972,550	122	0.05
Nigeria	1960	40,000,000	910,770	44	0.02
Poland	1960	28,000,000	119,874	234	0.10
Romania	1960	16,000,000	238,391	67	0.03
Soviet Union	1960	200,000,000	22,402,200	9	0.00
Tanzania	1960	10,000,000	944,303	11	0.00
Togo	1960	4,000,000	56,783	70	0.03
Tunisia	1960	4,000,000	163,610	24	0.01
U.S.S.R.	1960	200,000,000	22,402,200	9	0.00
Uganda	1960	10,000,000	241,038	41	0.02
Yugoslavia	1960	16,000,000	101,847	157	0.07

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